

SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 09:08:51 ; Search time 4393 Seconds
(without alignments)
10379.438 Million cell updates/sec

Title: US-09-903-771-1
Perfect score: 1052
Sequence: 1 tgcagcattgccggtggagc.....cctcttcgggccagtctgaa 1052

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
						<i>APPL.</i>
	1	1052	100.0	1052	6	AX377471 <i>WO 02/12291</i> Sequence
c	2	1052	100.0	309400	6	AX127153 <i>EP 1108790</i> Sequence
c	3	1052	100.0	325651	1	<u>AP005283</u> <i>GenBank</i> AP005283 Corynebac
	4	759	72.1	759	6	AX065953 <i>WO 01/00842</i> Sequence - <i>fragment</i>
	5	636	60.5	636	6	AX123320 <i>EP</i> Sequence
	6	636	60.5	636	6	BD165437 Novel pol
c	7	464	44.1	302070	1	AP005223 Corynebac
	8	404	38.4	1902	6	AX397915 Sequence
	9	404	38.4	1902	6	AX398211 Sequence
c	10	402.8	38.3	349659	1	BX248360 Corynebac
	11	353	33.6	353	6	AX377473 Sequence
	12	225	21.4	339650	1	SCO939108 Streptomy
	13	202.2	19.2	299050	1	SCO939119 Streptomy
	14	192.6	18.3	2760	1	SRSENRS Y14336 Streptomyce
	15	180.8	17.2	753	6	AX065957 Sequence
	16	180.8	17.2	760	6	AX763127 Sequence
	17	180.8	17.2	760	6	AX771859 Sequence
	18	180.8	17.2	1032	6	AX376724 Sequence
c	19	180.8	17.2	337200	1	AP005280 Corynebac
c	20	180.8	17.2	349980	6	AX127149 Sequence
c	21	180.8	17.2	349980	6	AX127150 Sequence
	22	178.4	17.0	630	6	AX122284 Sequence
	23	178.4	17.0	630	6	BD164401 Novel pol
	24	171.2	16.3	349659	1	BX248360 Corynebac
	25	164.8	15.7	2021	1	AF161327 Corynebac
	26	142	13.5	1498	6	AX763115 Sequence
	27	138.6	13.2	300100	1	SCO939123 Streptomy
	28	112	10.6	1311	6	AX123323 Sequence
	29	112	10.6	1311	6	BD165440 Novel pol
c	30	105.6	10.0	298450	1	SCO939107 Streptomy
	31	100.6	9.6	10542	1	AE001951 Deinococc
c	32	100	9.5	456	6	AX123319 Sequence
c	33	100	9.5	456	6	BD165436 Novel pol

Result	No.	Score	%		DB	ID		Description
			Query	Match Length				
c	1	1052	100.0	1052	6	ABA91930	wo 02/12291	Aba91930 Corynebac
	2	1052	100.0	309400	5	AAH68534	EP1108790	Aah68534 C glutami
	3	759	72.1	759	4	AAF71286	wo 01/0842	Aaf71286 Corynebac
	4	636	60.5	636	5	AAH68201		Aah68201 C glutami
	5	404	38.4	1902	6	ABL40476		Abl40476 C. glutam
	6	353	33.6	353	6	ABA91931		Aba91931 Corynebac
	7	180.8	17.2	753	4	AAF71288		Aaf71288 Corynebac
	8	180.8	17.2	760	9	ADD13670		Add13670 C. glutam

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 09:48:15 ; Search time 97 Seconds
(without alignments)
6018.643 Million cell updates/sec

Title: US-09-903-771-1
Perfect score: 1052
Sequence: 1 tgcagcattgccggtggagc.....cctcttcgggccagtctgaa 1052

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				
No.	Score	Query	Match	Length	ID	Description	
				DB			
1	180.8	17.2	1032	4	US-09-897-537A-1	Sequence 1, Appli	
2	84.2	8.0	323	4	US-09-897-537A-3	Sequence 3, Appli	
3	79.2	7.5	2588	2	US-08-796-414B-6	Sequence 6, Appli	
4	71.8	6.8	5045	3	US-09-390-721-1	Sequence 1, Appli	
5	71.8	6.8	5045	3	US-09-390-721-3	Sequence 3, Appli	
6	64	6.1	810	4	US-09-252-991A-3647	Sequence 3647, Ap	
7	64	6.1	879	4	US-09-252-991A-3602	Sequence 3602, Ap	
c 8	64	6.1	1632	4	US-09-252-991A-3859	Sequence 3859, Ap	
9	63	6.0	2766	4	US-09-252-991A-3756	Sequence 3756, Ap	
10	63	6.0	2874	4	US-09-252-991A-3837	Sequence 3837, Ap	
c 11	62.4	5.9	1515	4	US-09-252-991A-11671	Sequence 11671, A	
12	62.4	5.9	2232	4	US-09-252-991A-11756	Sequence 11756, A	

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 12:38:05 ; Search time 507 Seconds
(without alignments)
9385.965 Million cell updates/sec

Title: US-09-903-771-1
Perfect score: 1052
Sequence: 1 tgcagcattgccggtggagc.....cctcttcgggccagtctgaa 1052

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2936184 seqs, 2261732022 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	1052	100.0	1052	13	US-09-903-771-1	Sequence 322789,
c	2	1052	100.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
	3	636	60.5	636	9	US-09-738-626-3236	Sequence 3236, Ap
	4	404	38.4	1902	9	US-09-824-551-1	Sequence 1, Appli
	5	353	33.6	353	13	US-09-903-771-3	Sequence 3, Appli
	6	180.8	17.2	1032	10	US-09-867-537A-1	Sequence 1, Appli
	7	178.4	17.0	630	9	US-09-738-626-2200	Sequence 2200, Ap
	8	112	10.6	1311	9	US-09-738-626-3239	Sequence 3239, Ap
c	9	100	9.5	456	9	US-09-738-626-3235	Sequence 3235, Ap
c	10	96.6	9.2	9025608	15	US-10-156-761-1	Sequence 1, Appli
	11	89.8	8.5	663	15	US-10-156-761-1453	Sequence 1453, Ap
c	12	87	8.3	88421	9	US-09-976-059-1	Sequence 1, Appli
	13	85.2	8.1	9025608	15	US-10-156-761-1	Sequence 1, Appli
	14	84.2	8.0	323	10	US-09-867-537A-3	Sequence 3, Appli
	15	84.2	8.0	639	15	US-10-156-761-2864	Sequence 2864, Ap
	16	80.8	7.7	669	15	US-10-156-761-1976	Sequence 1976, Ap
	17	79	7.5	681	15	US-10-156-761-5587	Sequence 5587, Ap
	18	76.6	7.3	639	15	US-10-156-761-6454	Sequence 6454, Ap
	19	76.2	7.2	672	15	US-10-156-761-4519	Sequence 4519, Ap
	20	75.2	7.1	38734	10	US-09-373-658-30	Sequence 30, Appl
	21	75.2	7.1	38734	11	US-09-989-687-30	Sequence 30, Appl
	22	73.8	7.0	660	15	US-10-156-761-7049	Sequence 7049, Ap
	23	73.2	7.0	717	15	US-10-156-761-5606	Sequence 5606, Ap
	24	72.6	6.9	669	15	US-10-156-761-6649	Sequence 6649, Ap
	25	72.6	6.9	681	16	US-10-402-842-52	Sequence 52, Appl
c	26	72.6	6.9	47988	16	US-10-402-842-1	Sequence 1, Appli
	27	71.8	6.8	705	15	US-10-156-761-919	Sequence 919, App
	28	69.4	6.6	669	15	US-10-156-761-7370	Sequence 7370, Ap
	29	68.4	6.5	669	15	US-10-156-761-4665	Sequence 4665, Ap
	30	65.2	6.2	672	15	US-10-156-761-4521	Sequence 4521, Ap
	31	64.8	6.2	612	15	US-10-156-761-3119	Sequence 3119, Ap
	32	64.6	6.1	657	15	US-10-156-761-3617	Sequence 3617, Ap
	33	64.4	6.1	609	15	US-10-156-761-4982	Sequence 4982, Ap
	34	64.4	6.1	657	15	US-10-156-761-4359	Sequence 4359, Ap
	35	62.8	6.0	632	9	US-09-974-300-4335	Sequence 4335, Ap
	36	62.2	5.9	681	15	US-10-156-761-2425	Sequence 2425, Ap
	37	60.2	5.7	744	15	US-10-156-761-5052	Sequence 5052, Ap
	38	60.2	5.7	2061	9	US-09-738-626-2627	Sequence 2627, Ap
	39	60.2	5.7	3309400	9	US-09-738-626-1	Sequence 1, Appli
	40	58.2	5.5	660	15	US-10-156-761-2217	Sequence 2217, Ap
	41	55.6	5.3	630	15	US-10-156-761-5845	Sequence 5845, Ap
	42	53.8	5.1	3012	15	US-10-156-761-2716	Sequence 2716, Ap
	43	53.6	5.1	681	15	US-10-156-761-6016	Sequence 6016, Ap
	44	52	4.9	726	13	US-10-282-122A-7320	Sequence 7320, Ap
	45	52	4.9	726	13	US-10-389-647-221	Sequence 221, App

ALIGNMENTS

RESULT 1
US-09-903-771-1

Nakagawa
USFAP 2002/0197605

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 11:08:40 ; Search time 3219 Seconds
(without alignments)
9759.246 Million cell updates/sec

Title: US-09-903-771-1
Perfect score: 1052
Sequence: 1 tgcagcattgccggtggagc.....cctcttcgggccagtctgaa 1052

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	%		DB	ID	Description
			Query	Match Length			
c	1	63.2	6.0	1121	28	BZ578913	BZ578913 msh2_6062
c	2	62.4	5.9	994	28	BZ576614	BZ576614 msh2_5020
	3	62.4	5.9	1291	28	BZ559214	BZ559214 pacs2-164
c	4	62.4	5.9	1318	28	BZ579435	BZ579435 msh2_6354
	5	62.4	5.9	1351	28	BZ574737	BZ574737 msh2_382.
	6	60.8	5.8	788	28	BZ556373	BZ556373 pacs1-60_
	7	60.8	5.8	1312	28	BZ555372	BZ555372 pacs1-60_
c	8	59.4	5.6	1258	28	BZ573154	BZ573154 msh2_2968
	9	55.6	5.3	1200	28	BZ566682	BZ566682 pacs2-164
	10	51.8	4.9	203	14	H76739	H76739 17170 Lambd
c	11	51.8	4.9	529	9	AA898980	AA898980 NCM4D10T3
	12	50.4	4.8	714	28	BZ570280	BZ570280 msh2_1291
	13	50.4	4.8	1173	28	BZ552783	BZ552783 pacs1-60_
	14	49.6	4.7	678	28	AZ933822	AZ933822 BJ_Ba000
	15	49.2	4.7	1201	13	BX381961	BX381961 BX381961
	16	49	4.7	838	29	CG074421	CG074421 PUJGL44TD
	17	48.8	4.6	1132	28	BZ559201	BZ559201 pacs2-164
c	18	48.2	4.6	510	28	CC139486	CC139486 NDL.19M8.
c	19	48.2	4.6	670	14	CA258067	CA258067 SCCCRT300
c	20	48.2	4.6	782	29	CC867845	CC867845 NDL.52N16
c	21	47.8	4.5	712	13	BX416727	BX416727 BX416727
	22	47.8	4.5	1201	13	BX360624	BX360624 BX360624
c	23	47.2	4.5	1034	28	BZ559094	BZ559094 pacs2-164
	24	47	4.5	534	28	BZ293285	BZ293285 CG0247.r1
	25	47	4.5	1270	28	BZ576677	BZ576677 msh2_505.
c	26	46.6	4.4	601	13	CA144291	CA144291 SCRURT201
c	27	46.6	4.4	615	13	CA100770	CA100770 SCCCCL703
c	28	46.6	4.4	627	13	CA151391	CA151391 SCJFRZ200.
c	29	46.6	4.4	672	13	CA096378	CA096378 SCAGCL601.
c	30	46.6	4.4	703	13	BU102676	BU102676 SCCCAD100
c	31	46.6	4.4	703	13	CA064783	CA064783 SCCCAD100
c	32	46.2	4.4	796	28	BZ556455	BZ556455 pacs1-60_
c	33	45.6	4.3	896	28	BZ570242	BZ570242 msh2_126.
c	34	45.2	4.3	481	13	CA018544	CA018544 HV08O23r
	35	45.2	4.3	606	14	CA211255	CA211255 SCRLAD109
c	36	45.2	4.3	1046	28	AF035994	AF035994 AF035994
c	37	45	4.3	682	14	CA297537	CA297537 SCCCSD1C0
c	38	45	4.3	698	14	CA194718	CA194718 SCRFSB102
	39	45	4.3	1177	28	BZ559202	BZ559202 pacs2-164
c	40	44.8	4.3	580	14	CF649586	CF649586 3530_1_72
c	41	44.8	4.3	837	14	CF243426	CF243426 3530_1_21
	42	44.8	4.3	1201	13	BX340013	BX340013 BX340013
c	43	44.6	4.2	818	13	CA152415	CA152415 SCJFRZ202
c	44	44.6	4.2	885	13	BX425603	BX425603 BX425603
	45	44.6	4.2	1116	28	BZ551082	BZ551082 pacs1-60_

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 14:47:10 ; Search time 4393 Seconds
(without alignments)
10379.438 Million cell updates/sec

Title: US-09-903-771-1
Perfect score: 1052
Sequence: 1 tgcagcattgccggtggagc.....cctcttcgggccagtctgaa 1052

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*
- 15: em_ba:*
- 16: em_fun:*
- 17: em_hum:*
- 18: em_in:*
- 19: em_mu:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pat:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*

28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
	1	1052	100.0	1052	6	AX377471 <i>WO 02/12291</i>	AX377471 Sequence
c	2	1052	100.0	309400	6	AX127153 <i>EP 1108790</i>	AX127153 Sequence
c	3	1052	100.0	325651	1	<u>AP005283</u> <i>GenBank</i>	AP005283 Corynebac
	4	759	72.1	759	6	AX065953 <i>WO 01/00842</i>	AX065953 Sequence
	5	636	60.5	636	6	AX123320 <i>EP</i>	AX123320 Sequence
	6	636	60.5	636	6	BD165437 <i>JP 2002191370</i>	BD165437 Novel pol
	7	404	38.4	1902	6	AX397915 <i>WO 02/20777</i>	AX397915 Sequence
	8	404	38.4	1902	6	AX398211 <i>WO 02/20773</i>	AX398211 Sequence
	9	353	33.6	353	6	AX377473 <i>WO 02/12291</i>	AX377473 Sequence
	10	142	13.5	1498	6	AX763115 <i>WO 03/40181</i>	AX763115 Sequence
	11	112	10.6	1311	6	AX123323 <i>EP</i>	AX123323 Sequence
	12	112	10.6	1311	6	BD165440 <i>JP</i>	BD165440 Novel pol
c	13	100	9.5	456	6	AX123319 <i>EP</i>	AX123319 Sequence
c	14	100	9.5	456	6	BD165436 <i>JP</i>	BD165436 Novel pol
	15	23	2.2	1977	6	AX079001	AX079001 Sequence
c	16	23	2.2	305245	1	AE016793	AE016793 Pseudomon
c	17	23	2.2	347750	1	AP002998	AP002998 Mesorhizo
c	18	23	2.2	349659	1	BX248360	BX248360 Corynebac
	19	22	2.1	2021	1	AF161327	AF161327 Corynebac
	20	22	2.1	302007	1	SC0939132	AL939132 Streptomy
	21	22	2.1	349659	1	BX248360	BX248360 Corynebac
c	22	21	2.0	142133	2	AC135014	AC135014 Felis cat
	23	21	2.0	143092	3	CEY17G7B	AL023828 Caenorhab
c	24	21	2.0	158014	2	AC092413	AC092413 Felis cat
	25	21	2.0	181021	10	AL663031	AL663031 Mouse DNA
	26	21	2.0	262339	2	AC110265	AC110265 Mus muscu
	27	21	2.0	264291	2	AC104207	AC104207 Mus muscu
	28	21	2.0	299050	1	SC0939119	AL939119 Streptomy
	29	21	2.0	299550	1	AP005031	AP005031 Streptomy
c	30	21	2.0	302070	1	AP005223	AP005223 Corynebac
	31	20	1.9	13391	1	AE012389	AE012389 Xanthomon
c	32	20	1.9	123865	2	AC102005	AC102005 Mus muscu
c	33	20	1.9	142780	2	AC118735	AC118735 Mus muscu

OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 13:53:20 ; Search time 492 Seconds
(without alignments)
9083.545 Million cell updates/sec

Title: US-09-903-771-1
Perfect score: 1052
Sequence: 1 tgcagcattgccggtggagc.....cctcttcgggccagctctgaa 1052

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length	Match	Length			
	1	1052	100.0	1052	6	ABA91930	wo	02/12291	Aba91930 Corynebac
c	2	1052	100.0	309400	5	AAH68534	EP		Aah68534 C glutami
	3	759	72.1	759	4	AAF71286	wo	01/00842	Aaf71286 Corynebac
	4	636	60.5	636	5	AAH68201	EP		Aah68201 C glutami
	5	404	38.4	1902	6	ABL40476	wo	02/20799	Ab140476 C. glutam
	6	353	33.6	353	6	ABA91931	wo	02/12291	Aba91931 Corynebac
	7	142	13.5	1498	9	ADD13949	wo	03/40181	Add13949 C. glutam
	8	112	10.6	858	7	ACA01369	DE	10128510	Aca01369 C. glutam
	9	112	10.6	1311	5	AAH68204	EP		Aah68204 C glutami
c	10	100	9.5	456	5	AAH68200	EP		Aah68200 C glutami
c	11	100	9.5	456	7	ACA01348	DE		Aca01348 C. glutam
	12	23	2.2	1977	5	AAF26417			Aaf26417 Pseudomon

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 16:04:30 ; Search time 97 Seconds
(without alignments)
6018.643 Million cell updates/sec

Title: US-09-903-771-1
Perfect score: 1052
Sequence: 1 tgcagcattgccggtggagc.....cctcttcgggccagtctgaa 1052

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				ID	Description
	No.	Score	Match	Length	DB	Query		
	1	18	1.7	484	1	US-08-554-586-1		Sequence 1, Appli
	2	18	1.7	536165	4	US-09-214-808-1		Sequence 1, Appli
	3	17	1.6	444	4	US-09-252-991A-15154		Sequence 15154, A
c	4	17	1.6	465	4	US-09-252-991A-14734		Sequence 14734, A
	5	17	1.6	609	4	US-09-252-991A-15483		Sequence 15483, A
	6	17	1.6	621	4	US-09-252-991A-15020		Sequence 15020, A
	7	17	1.6	882	4	US-09-134-001C-2496		Sequence 2496, Ap
	8	17	1.6	1083	4	US-09-252-991A-15422		Sequence 15422, A
c	9	17	1.6	1221	4	US-09-489-039A-1479		Sequence 1479, Ap
c	10	17	1.6	1263	4	US-09-252-991A-2381		Sequence 2381, Ap
	11	17	1.6	1266	4	US-09-252-991A-14898		Sequence 14898, A
	12	17	1.6	1386	4	US-09-489-039A-4802		Sequence 4802, Ap

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 17:28:36 ; Search time 506 Seconds
(without alignments)
9404.514 Million cell updates/sec

Title: US-09-903-771-1
Perfect score: 1052
Sequence: 1 tgcagcattgccggtggagc.....cctcttcgggccagctctgaa 1052

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2936184 seqs, 2261732022 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1052	100.0	1052	13	US-09-903-771-1	Sequence 322789,
c 2	1052	100.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
3	636	60.5	636	9	US-09-738-626-3236	Sequence 3236, Ap
4	404	38.4	1902	9	US-09-824-551-1	Sequence 1, Appli
5	353	33.6	353	13	US-09-903-771-3	Sequence 3, Appli
6	112	10.6	1311	9	US-09-738-626-3239	Sequence 3239, Ap
c 7	100	9.5	456	9	US-09-738-626-3235	Sequence 3235, Ap
c 8	21	2.0	3138	15	US-10-156-761-2538	Sequence 2538, Ap
9	21	2.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
10	20	1.9	20	13	US-09-903-771-4	Sequence 4, Appli
c 11	20	1.9	20	13	US-09-903-771-5	Sequence 5, Appli
12	18	1.7	309	14	US-10-040-739-958	Sequence 958, App
c 13	18	1.7	404	13	US-10-027-632-183550	Sequence 183550,
c 14	18	1.7	404	13	US-10-027-632-183551	Sequence 183551,
c 15	18	1.7	404	16	US-10-027-632-183550	Sequence 183550,
c 16	18	1.7	404	16	US-10-027-632-183551	Sequence 183551,
17	18	1.7	439	9	US-09-867-701-5576	Sequence 5576, Ap
c 18	18	1.7	461	15	US-10-171-581-314	Sequence 314, App
19	18	1.7	584	13	US-10-425-114-9282	Sequence 9282, Ap
20	18	1.7	702	17	US-10-404-460-189	Sequence 189, App
c 21	18	1.7	806	13	US-10-027-632-170738	Sequence 170738,
c 22	18	1.7	806	13	US-10-027-632-170739	Sequence 170739,
c 23	18	1.7	806	16	US-10-027-632-170738	Sequence 170738,
c 24	18	1.7	806	16	US-10-027-632-170739	Sequence 170739,
25	18	1.7	909	13	US-10-424-599-60392	Sequence 60392, A
26	18	1.7	973	13	US-10-412-699B-983	Sequence 983, App
27	18	1.7	973	16	US-10-374-780A-482	Sequence 482, App
28	18	1.7	1158	15	US-10-156-761-1525	Sequence 1525, Ap
c 29	18	1.7	1778	13	US-10-424-599-40005	Sequence 40005, A
30	18	1.7	3154	14	US-10-044-090-38	Sequence 38, Appl
31	18	1.7	81684	13	US-10-087-192-145	Sequence 145, App
32	18	1.7	536165	10	US-09-939-964-1	Sequence 1, Appli
c 33	18	1.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
34	17	1.6	178	9	US-09-864-761-23453	Sequence 23453, A
35	17	1.6	339	16	US-10-062-674-1167	Sequence 1167, Ap
36	17	1.6	342	11	US-09-864-408A-1285	Sequence 1285, Ap
37	17	1.6	401	16	US-10-062-674-1250	Sequence 1250, Ap
38	17	1.6	448	13	US-10-424-599-138358	Sequence 138358,
39	17	1.6	491	9	US-09-867-701-620	Sequence 620, App
40	17	1.6	517	13	US-10-027-632-6974	Sequence 6974, Ap
41	17	1.6	517	16	US-10-027-632-6974	Sequence 6974, Ap
42	17	1.6	528	9	US-09-864-761-6719	Sequence 6719, Ap
43	17	1.6	568	15	US-10-029-386-1655	Sequence 1655, Ap
44	17	1.6	676	13	US-10-027-632-207363	Sequence 207363,
45	17	1.6	676	16	US-10-027-632-207363	Sequence 207363,

ALIGNMENTS

RESULT 1
US-09-903-771-1

USPAP 2002/0197605
USPAP 2002/0182687
LuxS-Gen
FD 4/4/01

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 15:55:45 ; Search time 3220 Seconds
(without alignments)
9756.216 Million cell updates/sec

Title: US-09-903-771-1
Perfect score: 1052
Sequence: 1 tgcagcattgccggtggagc.....cctcttcgggccagtctgaa 1052

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gssl:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	21	2.0	198	12	BM290466	BM290466 EST577000
	2	21	2.0	354	13	BY034863	BY034863 BY034863
c	3	21	2.0	444	13	BY590132	BY590132 BY590132
	4	21	2.0	487	12	BM291259	BM291259 EST577793
	5	21	2.0	748	12	BM292614	BM292614 EST575156
	6	21	2.0	1087	28	CC186660	CC186660 CH261-144
c	7	20	1.9	273	10	BF716978	BF716978 NcEST3a19
c	8	20	1.9	368	10	BB868867	BB868867 BB868867
c	9	20	1.9	417	14	CF838330	CF838330 UCRCS03_0
c	10	20	1.9	418	14	CF838670	CF838670 UCRCS03_0
	11	20	1.9	463	28	BH105940	BH105940 RPCI-24-4
	12	20	1.9	547	29	CG829255	CG829255 ZMMBBb035
c	13	20	1.9	565	12	BM624357	BM624357 170006874
c	14	20	1.9	568	12	BM610097	BM610097 170006871
	15	20	1.9	659	14	CB267786	CB267786 1006692 H
	16	20	1.9	971	12	BG701515	BG701515 602682751
	17	20	1.9	1090	29	CNS05R83	AL350220 Tetraodon
	18	19	1.8	57	14	CF297957	CF297957 7LEAF--01
	19	19	1.8	205	13	BY318076	BY318076 BY318076
	20	19	1.8	239	14	CF903433	CF903433 A0408G01-
	21	19	1.8	243	13	BY336988	BY336988 BY336988
c	22	19	1.8	308	9	AA363438	AA363438 EST73321
	23	19	1.8	309	10	BB120073	BB120073 BB120073
	24	19	1.8	331	9	AA375611	AA375611 EST88182
	25	19	1.8	331	13	BY343293	BY343293 BY343293
	26	19	1.8	333	13	BY315425	BY315425 BY315425
	27	19	1.8	336	13	BY319536	BY319536 BY319536
	28	19	1.8	336	13	BY337584	BY337584 BY337584
	29	19	1.8	338	13	BY145121	BY145121 BY145121
	30	19	1.8	339	14	CB076708	CB076708 hj43e03.g
	31	19	1.8	340	13	BY019055	BY019055 BY019055
	32	19	1.8	341	13	BY074549	BY074549 BY074549
	33	19	1.8	342	13	BY318539	BY318539 BY318539
	34	19	1.8	342	13	BY319902	BY319902 BY319902
	35	19	1.8	342	13	BY338237	BY338237 BY338237
	36	19	1.8	342	13	BY791814	BY791814 BY791814
	37	19	1.8	346	13	BY317192	BY317192 BY317192
	38	19	1.8	347	13	BY337231	BY337231 BY337231
	39	19	1.8	348	13	BY070017	BY070017 BY070017
	40	19	1.8	350	13	BY316095	BY316095 BY316095
	41	19	1.8	351	13	BY005304	BY005304 BY005304
	42	19	1.8	351	13	BY236832	BY236832 BY236832
	43	19	1.8	351	13	BY337404	BY337404 BY337404
	44	19	1.8	352	13	BY304931	BY304931 BY304931
	45	19	1.8	352	13	BY786914	BY786914 BY786914

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2004, 18:24:18 ; Search time 3728 Seconds
(without alignments)
2464.786 Million cell updates/sec

Title: US-09-903-771-2
Perfect score: 1030
Sequence: 1 MIRVLLADDHEIVRLGLRAV.....KLGVRRTSAVAAAREQGLL 212

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09903771/runat_30042004_082630_17729/app_query.fasta_1.3
91

-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09903771@CGN_1_1_3508@runat_30042004_082630_17729 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*

11: gb_sts:*
 12: gb_sy:*
 13: gb_un:*
 14: gb_vi:*
 15: em_ba:*
 16: em_fun:*
 17: em_hum:*
 18: em_in:*
 19: em_mu:*
 20: em_om:*
 21: em_or:*
 22: em_ov:*
 23: em_pat:*
 24: em_ph:*
 25: em_pl:*
 26: em_ro:*
 27: em_sts:*
 28: em_un:*
 29: em_vi:*
 30: em_htg_hum:*
 31: em_htg_inv:*
 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
 35: em_htg_rod:*
 36: em_htg_mam:*
 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	1030	100.0	636	6	AX123320	EP 1108790	AX123320	Sequence
	2	1030	100.0	636	6	BD165437	JP 2002191370	BD165437	Novel pol
	3	1030	100.0	759	6	AX065953	WO 01/00842	AX065953	Sequence
	4	1030	100.0	1052	6	AX377471	WO 02/12291	AX377471	Sequence
c	5	1030	100.0	309400	6	AX127153	EP	AX127153	Sequence
c	6	1030	100.0	325651	1	AP005283	GenBank	AP005283	Corynebac
c	7	994	96.5	302070	1	AP005223		AP005223	Corynebac
c	8	914	88.7	349659	1	BX248360		BX248360	Corynebac
	9	610	59.2	630	6	AX122284		AX122284	Sequence
	10	610	59.2	630	6	BD164401		BD164401	Novel pol
	11	610	59.2	753	6	AX065957		AX065957	Sequence
	12	610	59.2	760	6	AX763127		AX763127	Sequence
	13	610	59.2	760	6	AX771859		AX771859	Sequence
	14	610	59.2	1032	6	AX376724		AX376724	Sequence
c	15	610	59.2	337200	1	AP005280		AP005280	Corynebac
c	16	610	59.2	349980	6	AX127149		AX127149	Sequence

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2004, 18:22:31 ; Search time 387 Seconds
(without alignments)
2327.178 Million cell updates/sec

Title: US-09-903-771-2
Perfect score: 1030
Sequence: 1 MIRVLLADDHEIVRLGLRAV.....KLGVRRTSAVAAAREQGLL 212

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-

Q=/cgn2_1/USPTO_spool/US09903771/runat_30042004_082630_17719/app_query.fasta_1.3
91

-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09903771 @CGN_1_1_470 @runat_30042004_082630_17719 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	1030	100.0	636	5	AAH68201	Aah68201 C glutami
	2	1030	100.0	759	4	AAF71286	Aaf71286 Corynebac
	3	1030	100.0	1052	6	ABA91930	Aba91930 Corynebac
c	4	1030	100.0	309400	5	AAH68534	Aah68534 C glutami
	5	610	59.2	630	5	AAH67165	Aah67165 C glutami
	6	610	59.2	753	4	AAF71288	Aaf71288 Corynebac
	7	610	59.2	760	9	ADD13670	Add13670 C. glutam
	8	610	59.2	760	9	ADD13961	Add13961 C. glutam
	9	610	59.2	1032	6	ABA95154	Aba95154 C. glutam
c	10	610	59.2	349980	5	AAH68531	Aah68531 C glutami
c	11	610	59.2	349980	5	AAH68530	Aah68530 C glutami
	12	577	56.0	353	6	ABA91931	Aba91931 Corynebac
	13	525	51.0	12531	4	AAS59530	Aas59530 Propionib
	14	525	51.0	12531	7	ACF64459	Acf64459 Propionib
	15	390.5	37.9	23474	4	AAS59511	Aas59511 Propionib
	16	390.5	37.9	23474	7	ACF64440	Acf64440 Propionib
	17	387	37.6	632	6	ABK77044	Abk77044 Bacillus
	18	379.5	36.8	38726	4	AAS59513	Aas59513 Propionib
	19	379.5	36.8	38726	7	ACF64442	Acf64442 Propionib
c	20	375.5	36.5	88421	6	AAL40781	Aal40781 88421nt g
c	21	373.5	36.3	47988	9	ADE86070	Ade86070 Streptomy
	22	358.5	34.8	2538	2	AAX21398	Aax21398 Central f
	23	350.5	34.0	10391	2	AAX13070	Aax13070 Enterococ
	24	350.5	34.0	10391	6	ABS98865	Abs98865 Enterococ
	25	344.5	33.4	110000	6	ABQ69245_10	Continuation (11 o
	26	344.5	33.4	110000	6	ABQ67197_09	Continuation (10 o
c	27	343.5	33.3	5944	4	AAS59604	Aas59604 Propionib
c	28	343.5	33.3	5944	7	ACF64533	Acf64533 Propionib
	29	343.5	33.3	110000	6	ABA03041_10	Continuation (11 o
c	30	342	33.2	1373	4	AAS59700	Aas59700 Propionib
c	31	342	33.2	1373	7	ACF64629	Acf64629 Propionib
	32	342	33.2	66788	4	AAS59515	Aas59515 Propionib
	33	342	33.2	66788	7	ACF64444	Acf64444 Propionib
	34	341.5	33.2	639	9	ADC93578	Adc93578 E. faeciu
	35	341	33.1	84707	6	ABQ67196_6	Continuation (7 of
	36	341	33.1	110000	6	ABQ67196_5	Continuation (6 of
c	37	341	33.1	110000	6	ABQ69245_26	Continuation (27 o
c	38	341	33.1	110000	6	ABA03041_25	Continuation (26 o
	39	340.5	33.1	1251	6	ABQ69042	Abq69042 Listeria
	40	340.5	33.1	4403	6	ABQ70942	Abq70942 Listeria
c	41	338.5	32.9	17083	7	ABZ58812	Abz58812 S. cinnam
	42	330.5	32.1	648	8	ADB10145	Adb10145 Alloiococ
c	43	330.5	32.1	110000	8	ADB12064_12	Continuation (13 o
c	44	330.5	32.1	110000	8	ADB12064_13	Continuation (14 o
	45	328.5	31.9	648	6	ABN92436	Abn92436 Staphyloc

ALIGNMENTS

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2004, 19:44:12 ; Search time 78 Seconds
(without alignments)
1508.328 Million cell updates/sec

Title: US-09-903-771-2
Perfect score: 1030
Sequence: 1 MIRVLLADDHEIVRLGLRAV.....KLGVRRTSAVAAAREQGLL 212

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-

Q=/cgn2_1/USPTO_spool/US09903771/runat_30042004_082631_17783/app_query.fasta_1.3
91

-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09903771@cgn2_1_1_56@runat_30042004_082631_17783 -NCPUs=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query		Length	DB	ID	Description
	No.	Score Match				
	1	610 59.2	1032	4	US-09-897-537A-1	Sequence 1, Appli
	2	376 36.5	5045	3	US-09-390-721-1	Sequence 1, Appli
	3	376 36.5	5045	3	US-09-390-721-3	Sequence 3, Appli
	4	358.5 34.8	2588	2	US-08-796-414B-6	Sequence 6, Appli
	5	350.5 34.0	648	4	US-09-134-000C-1163	Sequence 1163, Ap
	6	341.5 33.2	639	4	US-09-107-532A-3205	Sequence 3205, Ap
	7	331.5 32.2	810	4	US-09-252-991A-3647	Sequence 3647, Ap
	8	331.5 32.2	879	4	US-09-252-991A-3602	Sequence 3602, Ap
c	9	331.5 32.2	1632	4	US-09-252-991A-3859	Sequence 3859, Ap
	10	328.5 31.9	648	4	US-09-134-001C-1899	Sequence 1899, Ap
c	11	328 31.8	1830121	4	US-09-557-884-1	Sequence 1, Appli
c	12	328 31.8	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	13	323.5 31.4	900	2	US-08-771-784-1	Sequence 1, Appli
	14	323.5 31.4	900	3	US-09-076-756-1	Sequence 1, Appli
c	15	323.5 31.4	3334	3	US-09-255-984-1	Sequence 1, Appli
	16	308.5 30.0	1419	4	US-08-956-171E-438	Sequence 438, App
	17	308 29.9	1666	1	US-08-848-932-1	Sequence 1, Appli
	18	308 29.9	1666	2	US-09-008-180-1	Sequence 1, Appli
c	19	308 29.9	11887	4	US-08-961-527-146	Sequence 146, App
	20	306.5 29.8	702	4	US-09-489-039A-3142	Sequence 3142, Ap
	21	306 29.7	323	4	US-09-897-537A-3	Sequence 3, Appli
c	22	306 29.7	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	23	306 29.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	24	305.5 29.7	7965	4	US-08-956-171E-321	Sequence 321, App
	25	302.5 29.4	705	4	US-09-543-681A-2052	Sequence 2052, Ap
	26	295 28.6	840	4	US-09-651-656-106	Sequence 106, App
	27	295 28.6	840	4	US-09-650-855-106	Sequence 106, App
	28	294.5 28.6	636	4	US-09-134-001C-976	Sequence 976, App
c	29	292 28.3	5014	3	US-09-381-862-3	Sequence 3, Appli
	30	288 28.0	660	4	US-09-543-681A-3866	Sequence 3866, Ap
	31	287.5 27.9	678	4	US-09-252-991A-794	Sequence 794, App
c	32	287.5 27.9	2577	4	US-09-252-991A-828	Sequence 828, App
	33	284.5 27.6	777	4	US-09-540-236-1792	Sequence 1792, Ap
c	34	284.5 27.6	63563	4	US-09-596-002-33	Sequence 33, Appl
	35	280 27.2	711	4	US-09-489-039A-7022	Sequence 7022, Ap
	36	268.5 26.1	642	2	US-09-009-218-9	Sequence 9, Appli
	37	263.5 25.6	642	1	US-08-761-258-9	Sequence 9, Appli
	38	263.5 25.6	642	2	US-09-009-218-7	Sequence 7, Appli
	39	263.5 25.6	642	2	US-08-977-306-9	Sequence 9, Appli
	40	262.5 25.5	642	1	US-08-761-258-4	Sequence 4, Appli
	41	262.5 25.5	642	2	US-08-977-306-4	Sequence 4, Appli
	42	262 25.4	663	4	US-09-252-991A-14645	Sequence 14645, A
c	43	262 25.4	2769	4	US-09-252-991A-15111	Sequence 15111, A
	44	261.5 25.4	642	2	US-09-009-218-3	Sequence 3, Appli
	45	260.5 25.3	771	4	US-09-328-352-1304	Sequence 1304, Ap

ALIGNMENTS

RESULT 1

US-09-897-537A-1

; Sequence 1, Application US/09897537A

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2004, 20:56:22 ; Search time 406 Seconds
(without alignments)
2362.006 Million cell updates/sec

Title: US-09-903-771-2
Perfect score: 1030
Sequence: 1 MIRVLLADDHEIVRLGLRAV.....KLGVRRTSAVAAAAREQGLL 212

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2936184 seqs, 2261732022 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09903771/runat_30042004_082632_17833/app_query.fasta_1.3
91

-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09903771 @CGN_1_1_221 @runat_30042004_082632_17833
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%						Description
	No.	Score	Query Match	Length	DB	ID	
	1	1030	100.0	636	9	US-09-738-626-3236	Sequence 3236, Ap
	2	1030	100.0	1052	13	US-09-903-771-1	Sequence 322789,
c	3	1030	100.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
	4	610	59.2	630	9	US-09-738-626-2200	Sequence 2200, Ap
	5	610	59.2	1032	10	US-09-867-537A-1	Sequence 1, Appli
	6	577	56.0	353	13	US-09-903-771-3	Sequence 3, Appli
	7	409.5	39.8	669	15	US-10-156-761-6649	Sequence 6649, Ap
c	8	409.5	39.8	9025608	15	US-10-156-761-1	Sequence 1, Appli
	9	398	38.6	660	15	US-10-156-761-7049	Sequence 7049, Ap
	10	389.5	37.8	744	15	US-10-156-761-5052	Sequence 5052, Ap
	11	389.5	37.8	9025608	15	US-10-156-761-1	Sequence 1, Appli
	12	388	37.7	669	15	US-10-156-761-4665	Sequence 4665, Ap
	13	387	37.6	632	9	US-09-974-300-4335	Sequence 4335, Ap
	14	385	37.4	681	15	US-10-156-761-5587	Sequence 5587, Ap
	15	381.5	37.0	639	15	US-10-156-761-6454	Sequence 6454, Ap
	16	376	36.5	705	15	US-10-156-761-919	Sequence 919, App
c	17	375.5	36.5	88421	9	US-09-976-059-1	Sequence 1, Appli
	18	373.5	36.3	681	16	US-10-402-842-52	Sequence 52, Appl
c	19	373.5	36.3	47988	16	US-10-402-842-1	Sequence 1, Appli
	20	368.5	35.8	663	15	US-10-156-761-1453	Sequence 1453, Ap
	21	365.5	35.5	717	15	US-10-156-761-5606	Sequence 5606, Ap
	22	360	35.0	639	15	US-10-156-761-2864	Sequence 2864, Ap
	23	356.5	34.6	672	15	US-10-156-761-4521	Sequence 4521, Ap
	24	354.5	34.4	672	15	US-10-156-761-4519	Sequence 4519, Ap
	25	350.5	34.0	10391	9	US-09-070-927A-133	Sequence 133, App
	26	344.5	33.4	1163020	16	US-10-398-221-10	Sequence 10, Appl
	27	344.5	33.4	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
	28	341	33.1	684707	16	US-10-398-221-9	Sequence 9, Appli
c	29	341	33.1	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
	30	340.5	33.1	1251	16	US-10-398-221-1855	Sequence 1855, Ap
	31	340.5	33.1	4403	16	US-10-398-221-3755	Sequence 3755, Ap
	32	338	32.8	669	15	US-10-156-761-1976	Sequence 1976, Ap
	33	338	32.8	681	15	US-10-156-761-2425	Sequence 2425, Ap
	34	335.5	32.6	657	15	US-10-156-761-4359	Sequence 4359, Ap
	35	333.5	32.4	648	15	US-10-156-761-4438	Sequence 4438, Ap
	36	333.5	32.4	681	15	US-10-156-761-6016	Sequence 6016, Ap
	37	328.5	31.9	612	15	US-10-156-761-3119	Sequence 3119, Ap
c	38	328	31.8	1830121	15	US-10-329-960-1	Sequence 1, Appli
c	39	328	31.8	1830121	16	US-10-329-670-1	Sequence 1, Appli

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2004, 19:32:57 ; Search time 2496 Seconds
(without alignments)
2536.371 Million cell updates/sec

Title: US-09-903-771-2
Perfect score: 1030
Sequence: 1 MIRVLLADDHEIVRLGLRAV.....KLGVRSRSAVAAAAREQGLL 212

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09903771/runat_30042004_082630_17758/app_query.fasta_1.3
91

-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09903771 @CGN_1_1_2810 @runat_30042004_082630_17758 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*

12: gb_est3:*
 13: gb_est4:*
 14: gb_est5:*
 15: em_estfun:*
 16: em_estom:*
 17: em_gss_hum:*
 18: em_gss_inv:*
 19: em_gss_pln:*
 20: em_gss_vrt:*
 21: em_gss_fun:*
 22: em_gss_mam:*
 23: em_gss_mus:*
 24: em_gss_pro:*
 25: em_gss_rod:*
 26: em_gss_phg:*
 27: em_gss_vrl:*
 28: gb_gss1:*
 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES									
Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
c	1	328.5	31.9	782	29	CC867845			CC867845 NDL.52N16
c	2	296.5	28.8	1258	28	BZ573154			BZ573154 msh2_2968
	3	258	25.0	534	28	BZ293285			BZ293285 CG0247.r1
c	4	226.5	22.0	510	28	CC139486			CC139486 NDL.19M8.
	5	226.5	22.0	609	10	BF637659			BF637659 NF041B10P
	6	223	21.7	639	10	BF637779			BF637779 NF041E11P
c	7	218.5	21.2	820	28	BZ559345			BZ559345 pacs2-164
c	8	217.5	21.1	795	28	BZ574576			BZ574576 msh2_3734
c	9	204	19.8	1048	28	BZ561394			BZ561394 pacs2-164
	10	200.5	19.5	1363	28	BZ572628			BZ572628 msh2_2725
c	11	197.5	19.2	1286	28	BZ575802			BZ575802 msh2_4633
	12	194.5	18.9	1053	28	BZ567061			BZ567061 pacs2-164
	13	192.5	18.7	1010	28	BZ679460			BZ679460 PUBDJ52TD
	14	188	18.3	1132	28	BZ559201			BZ559201 pacs2-164
	15	184	17.9	931	28	BZ568400			BZ568400 pacs2-164
	16	182.5	17.7	1186	28	BZ550497			BZ550497 pacs1-60_
	17	181.5	17.6	1116	28	BZ551082			BZ551082 pacs1-60_
c	18	179	17.4	890	28	BZ556529			BZ556529 pacs1-60_
	19	178.5	17.3	668	28	BZ548552			BZ548552 pacs1-60_
	20	174.5	16.9	1173	28	BZ568225			BZ568225 pacs2-164
	21	173.5	16.8	1270	28	BZ576677			BZ576677 msh2_505.
c	22	169	16.4	782	28	AZ934050			AZ934050 BJ__Ba000
	23	169	16.4	805	28	BH399199			BH399199 AG-ND-175
	24	168	16.3	466	14	CD143606			CD143606 MG1-0086T
	25	167	16.2	1144	28	BZ560680			BZ560680 pacs2-164
c	26	166.5	16.2	994	28	BZ576614			BZ576614 msh2_5020
	27	165.5	16.1	788	28	BZ556373			BZ556373 pacs1-60_
	28	164.5	16.0	578	29	CNS07GQ1			AL610075 Anopheles
	29	163	15.8	826	28	BZ573644			BZ573644 msh2_3292